SEQUENCE LISTING

<110> Staunton, Donald E.

<120> MATERIALS AND METHODS TO MODULATE LIGAND BINDING/ENZYMATIC ACTIVITY OF ALPHA/BETA PROTEINS CONTAINING AN ALLOSTERIC REGULATORY SITE

<130> 27866/36470A

<140> 09/976,935

<141> 2001-10-12

<150> US 60/239,750

<151> 2000-10-12

<160> 36

<170> PatentIn version 3.1

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Pro Lys Gly Arg His Arg Gly Val Thr Val Val Arg Ser His His Gly
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Val Leu Ile Cys Ile Gln Val Leu Val Arg Arg
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gaggggaagc ttagtgggcc 20

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<213> amino acid sequence of ???

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Met Thr Val Ala Tyr Ile Ala Ile Gly Ser Asn Leu Ala Ser Pro Leu
1 5 10 15

Glu Gln Val Asn Ala Ala Leu Lys Ala Leu Gly Asp Ile Pro Glu Ser
20 25 30

His Ile Leu Thr Val Ser Ser Phe Tyr Arg Thr Pro Pro Leu Gly Pro
35 40 45

Gln Asp Gln Pro Asp Tyr Leu Asn Ala Ala Val Ala Leu Glu Thr Ser
50 55 60

Leu Ala Pro Glu Glu Leu Leu Asn His Thr Gln Arg Ile Glu Leu Gln
65 70 75 80

Gln Gly Arg Val Arg Lys Ala Glu Arg Trp Gly Pro Arg Thr Leu Asp
85 90 95

Leu Asp Ile Met Leu Phe Gly Asn Glu Val Ile Asn Thr Glu Arg Leu
100 105 110

Thr Val Pro His Tyr Asp Met Lys Asn Arg Gly Phe Met Leu Trp Pro
115 120 125

Leu Phe Glu Ile Ala Pro Glu Leu Val Phe Pro Asp Gly Glu Met Leu
130 135 140

Arg Gln Ile Leu His Thr Arg Ala Phe Asp Lys Leu Asn Lys Trp
145 150 155

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<213> ????

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Met Gly His His His His His His Gly Gly
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<213> 3'EcXhoHPPK

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<212> PRT

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Ala Ile Gly Ser Asn Leu Ala Ser Pro Leu Glu Gln Val Asn Ala Ala
20 25 30

Leu Lys Ala Leu Gly Asp Ile Pro Glu Ser His Ile Leu Thr Val Ser
35 40 45

Ser Phe Tyr Arg Thr Pro Pro Leu Gly Pro Gln Asp Gln Pro Asp Tyr
50 55 60

Leu Asn Ala Ala Val Ala Leu Glu Thr Ser Leu Ala Pro Glu Glu Leu
65 70 75 80

Leu Asn His Thr Gln Arg Ile Glu Leu Gln Gln Gly Arg Val Arg Lys
85 90 95

Ala Glu Arg Trp Gly Pro Arg Thr Leu Asp Leu Asp Ile Met Leu Phe
100 105 110

Gly Asn Glu Val Ile Asn Thr Glu Arg Leu Thr Val Pro His Tyr Asp
115 120 125

Met Lys Asn Arg Gly Phe Met Leu Trp Pro Leu Phe Glu Ile Ala Pro
130 135 140

Glu Leu Val Phe Pro Asp Gly Glu Met Leu Arg Gln Ile Leu His Thr
145 150 155 160

Arg Ala Phe Asp Lys Leu Asn Lys Trp
165

<210> 35

<211> 180

<212> PRT

<213> amino acid sequence of LFA-1 I domain

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Gly Asn Val Asp Leu Val Phe Leu Phe Asp Gly Ser Met Ser Leu Gln
1 5 10 15

Pro Asp Glu Phe Gln Lys Ile Leu Asp Phe Met Lys Asp Val Met Lys
20 25 30

Lys Leu Ser Asn Thr Ser Tyr Gln Phe Ala Ala Val Gln Phe Ser Thr
35 40 45

Ser Tyr Lys Thr Glu Phe Asp Phe Ser Asp Tyr Val Lys Trp Lys Asp
50 55 60

Pro Asp Ala Leu Leu Lys His Val Lys His Met Leu Leu Leu Thr Asn
65 70 75 80

Thr Phe Gly Ala Ile Asn Tyr Val Ala Thr Glu Val Phe Arg Glu Glu
85 90 95

Leu Gly Ala Arg Pro Asp Ala Thr Lys Val Leu Ile Ile Ile Thr Asp
100 105 110

Gly Glu Ala Thr Asp Ser Gly Asn Ile Asp Ala Ala Lys Asp Ile Ile
115 120 125

Arg Tyr Ile Ile Gly Ile Gly Lys His Phe Gln Thr Lys Glu Ser Gln
130 135 140

Glu Thr Leu His Lys Phe Ala Ser Lys Pro Ala Ser Glu Phe Val Lys
145 150 155 160

Ile Leu Asp Thr Phe Glu Lys Leu Lys Asp Leu Phe Thr Glu Leu Gln
165 170 175

Lys Lys Ile Tyr
180

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<213> amino acid sequence of LFA-1

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Met Lys Asp Ser Cys Ile Thr Val Met Ala Met Ala Leu Leu Ser Gly
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Phe Phe Phe Phe Ala Pro Ala Ser Ser Tyr Asn Leu Asp Val Arg Gly
20 25 30

Ala Arg Ser Phe Ser Pro Pro Arg Ala Gly Arg His Phe Gly Tyr Arg
35 40 45

Val Leu Gln Val Gly Asn Gly Val Ile Val Gly Ala Pro Gly Glu Gly
50 55 60

Asn Ser Thr Gly Ser Leu Tyr Gln Cys Gln Ser Gly Thr Gly His Cys
65 70 75 80

Leu Pro Val Thr Leu Arg Gly Ser Asn Tyr Thr Ser Lys Tyr Leu Gly
85 90 95

Met Thr Leu Ala Thr Asp Pro Thr Asp Gly Ser Ile Leu Ala Cys Asp
100 105 110

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Pro Gly Leu Ser Arg Thr Cys Asp Gln Asn Thr Tyr Leu Ser Gly Leu
        115                 120                 125

Cys Tyr Leu Phe Arg Gln Asn Leu Gln Gly Pro Met Leu Gln Gly Arg
    130                 135                 140

Pro Gly Phe Gln Glu Cys Ile Lys Gly Asn Val Asp Leu Val Phe Leu
145                 150                 155                 160

Phe Asp Gly Ser Met Ser Leu Gln Pro Asp Glu Phe Gln Lys Ile Leu
                165                 170                 175

Asp Phe Met Lys Asp Val Met Lys Lys Leu Ser Asn Thr Ser Tyr Gln
            180                 185                 190

Phe Ala Ala Val Gln Phe Ser Thr Ser Tyr Lys Thr Glu Phe Asp Phe
        195                 200                 205

Ser Asp Tyr Val Lys Trp Lys Asp Pro Asp Ala Leu Leu Lys His Val
    210                 215                 220

Lys His Met Leu Leu Leu Thr Asn Thr Phe Gly Ala Ile Asn Tyr Val
225                 230                 235                 240

Ala Thr Glu Val Phe Arg Glu Glu Leu Gly Ala Arg Pro Asp Ala Thr
                245                 250                 255

Lys Val Leu Ile Ile Ile Thr Asp Gly Glu Ala Thr Asp Ser Gly Asn
            260                 265                 270

Ile Asp Ala Ala Lys Asp Ile Ile Arg Tyr Ile Ile Gly Ile Gly Lys
        275                 280                 285

His Phe Gln Thr Lys Glu Ser Gln Glu Thr Leu His Lys Phe Ala Ser
    290                 295                 300

Lys Pro Ala Ser Glu Phe Val Lys Ile Leu Asp Thr Phe Glu Lys Leu
305                 310                 315                 320

Lys Asp Leu Phe Thr Glu Leu Gln Lys Lys Ile Tyr Val Ile Glu Gly
                325                 330                 335

Thr Ser Lys Gln Asp Leu Thr Ser Phe Asn Met Glu Leu Ser Ser Ser
            340                 345                 350

Gly Ile Ser Ala Asp Leu Ser Arg Gly His Ala Val Val Gly Ala Val
        355                 360                 365
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Gly Ala Lys Asp Trp Ala Gly Gly Phe Leu Asp Leu Lys Ala Asp Leu
    370                 375                 380

Gln Asp Asp Thr Phe Ile Gly Asn Glu Pro Leu Thr Pro Glu Val Arg
385                 390                 395                 400

Ala Gly Tyr Leu Gly Tyr Thr Val Thr Trp Leu Pro Ser Arg Gln Lys
                405                 410                 415

Thr Ser Leu Leu Ala Ser Gly Ala Pro Arg Tyr Gln His Met Gly Arg
            420                 425                 430

Val Leu Leu Phe Gln Glu Pro Gln Gly Gly Gly His Trp Ser Gln Val
        435                 440                 445

Gln Thr Ile His Gly Thr Gln Ile Gly Ser Tyr Phe Gly Gly Glu Leu
    450                 455                 460

Cys Gly Val Asp Val Asp Gln Asp Gly Glu Thr Glu Leu Leu Leu Ile
465                 470                 475                 480

Gly Ala Pro Leu Phe Tyr Gly Glu Gln Arg Gly Gly Arg Val Phe Ile
                485                 490                 495

Tyr Gln Arg Arg Gln Leu Gly Phe Glu Glu Val Ser Glu Leu Gln Gly
            500                 505                 510

Asp Pro Gly Tyr Pro Leu Gly Arg Phe Gly Glu Ala Ile Thr Ala Leu
        515                 520                 525

Thr Asp Ile Asn Gly Asp Gly Leu Val Asp Val Ala Val Gly Ala Pro
    530                 535                 540

Leu Glu Glu Gln Gly Ala Val Tyr Ile Phe Asn Gly Arg His Gly Gly
545                 550                 555                 560

Leu Ser Pro Gln Pro Ser Gln Arg Ile Glu Gly Thr Gln Val Leu Ser
                565                 570                 575

Gly Ile Gln Trp Phe Gly Arg Ser Ile His Gly Val Lys Asp Leu Glu
            580                 585                 590

Gly Asp Gly Leu Ala Asp Val Ala Val Gly Ala Glu Ser Gln Met Ile
        595                 600                 605

Val Leu Ser Ser Arg Pro Val Val Asp Met Val Thr Leu Met Ser Phe
    610                 615                 620
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Ser Pro Ala Glu Ile Pro Val His Glu Val Glu Cys Ser Tyr Ser Thr
625                 630                 635                 640

Ser Asn Lys Met Lys Glu Gly Val Asn Ile Thr Ile Cys Phe Gln Ile
                645                 650                 655

Lys Ser Leu Tyr Pro Gln Phe Gln Gly Arg Leu Val Ala Asn Leu Thr
            660                 665                 670

Tyr Thr Leu Gln Leu Asp Gly His Arg Thr Arg Arg Arg Gly Leu Phe
        675                 680                 685

Pro Gly Gly Arg His Glu Leu Arg Arg Asn Ile Ala Val Thr Thr Ser
    690                 695                 700

Met Ser Cys Thr Asp Phe Ser Phe His Phe Pro Val Cys Val Gln Asp
705                 710                 715                 720

Leu Ile Ser Pro Ile Asn Val Ser Leu Asn Phe Ser Leu Trp Glu Glu
                725                 730                 735

Glu Gly Thr Pro Arg Asp Gln Arg Ala Gln Gly Lys Asp Ile Pro Pro
            740                 745                 750

Ile Leu Arg Pro Ser Leu His Ser Glu Thr Trp Glu Ile Pro Phe Glu
        755                 760                 765

Lys Asn Cys Gly Glu Asp Lys Lys Cys Glu Ala Asn Leu Arg Val Ser
    770                 775                 780

Phe Ser Pro Ala Arg Ser Arg Ala Leu Arg Leu Thr Ala Phe Ala Ser
785                 790                 795                 800

Leu Ser Val Glu Leu Ser Leu Ser Asn Leu Glu Glu Asp Ala Tyr Trp
                805                 810                 815

Val Gln Leu Asp Leu His Phe Pro Pro Gly Leu Ser Phe Arg Lys Val
            820                 825                 830

Glu Met Leu Lys Pro His Ser Gln Ile Pro Val Ser Cys Glu Glu Leu
        835                 840                 845

Pro Glu Glu Ser Arg Leu Leu Ser Arg Ala Leu Ser Cys Asn Val Ser
    850                 855                 860

Ser Pro Ile Phe Lys Ala Gly His Ser Val Ala Leu Gln Met Met Phe
865                 870                 875                 880
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Asn Thr Leu Val Asn Ser Ser Trp Gly Asp Ser Val Glu Leu His Ala
                885                 890                 895

Asn Val Thr Cys Asn Asn Glu Asp Ser Asp Leu Leu Glu Asp Asn Ser
            900                 905                 910

Ala Thr Thr Ile Ile Pro Ile Leu Tyr Pro Ile Asn Ile Leu Ile Gln
        915                 920                 925

Asp Gln Glu Asp Ser Thr Leu Tyr Val Ser Phe Thr Pro Lys Gly Pro
    930                 935                 940

Lys Ile His Gln Val Lys His Met Tyr Gln Val Arg Ile Gln Pro Ser
945                 950                 955                 960

Ile His Asp His Asn Ile Pro Thr Leu Glu Ala Val Val Gly Val Pro
                965                 970                 975

Gln Pro Pro Ser Glu Gly Pro Ile Thr His Gln Trp Ser Val Gln Met
            980                 985                 990

Glu Pro Pro Val Pro Cys His Tyr  Glu Asp Leu Glu Arg  Leu Pro Asp
        995                 1000                1005

Ala Ala  Glu Pro Cys Leu Pro  Gly Ala Leu Phe Arg  Cys Pro Val
    1010                1015                1020

Val Phe  Arg Gln Glu Ile Leu  Val Gln Val Ile Gly  Thr Leu Glu
    1025                1030                1035

Leu Val  Gly Glu Ile Glu Ala  Ser Ser Met Phe Ser  Leu Cys Ser
    1040                1045                1050

Ser Leu  Ser Ile Ser Phe Asn  Ser Ser Lys His Phe  His Leu Tyr
    1055                1060                1065

Gly Ser  Asn Ala Ser Leu Ala  Gln Val Val Met Lys  Val Asp Val
    1070                1075                1080

Val Tyr  Glu Lys Gln Met Leu  Tyr Leu Tyr Val Leu  Ser Gly Ile
    1085                1090                1095

Gly Gly  Leu Leu Leu Leu Leu  Leu Ile Phe Ile Val  Leu Tyr Lys
    1100                1105                1110

Val Gly  Phe Phe Lys Arg Asn  Leu Lys Glu Lys Met  Glu Ala Gly
    1115                1120                1125
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Arg Gly  Val Pro Asn Gly Ile  Pro Ala Glu Asp Ser  Glu Gln Leu
    1130                 1135                 1140

Ala Ser  Gly Gln Glu Ala Gly  Asp Pro Gly Cys Leu  Lys Pro Leu
    1145                 1150                 1155

His Glu  Lys Asp Ser Glu Ser  Gly Gly Gly Lys Asp
    1160                 1165                 1170
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